

Features of Human Slit-1 predicted protein
Co-ordinates refer to amino acid number.

Signal sequence:	7-24
First amino-flanking sequence:	28-59
First set of Leucine Rich Repeats:	60-179
First carboxy-flanking sequence:	180-276
Second amino-flanking sequence:	277-308
Second set of Leucine Rich Repeats:	309-434
Second carboxy-flanking sequence:	435-501
Third amino-flanking sequence:	502-533
Third set of Leucine Rich Repeats:	534-660
Third carboxy-flanking sequence:	661-722
Fourth amino-flanking sequence:	723-754
Fourth set of Leucine Rich Repeats:	755-855
Fourth carboxy-flanking sequence:	856-917
First EGF repeat:	918-952
Second EGF repeat:	953-993
Third EGF repeat:	994-1031
Fourth EGF repeat:	1032-1071
Fifth EGF repeat:	1072-1109
Spacer:	1110-1116
Sixth EGF repeat:	1117-1154
"99aa spacer":	1155-1329
Seventh EGF repeat:	1330-1366
Eighth EGF repeat:	1367-1404
Nineth EGF repeat:	1405-1447
Cysteine knot motif:	1448-1525

Leucine rich repeats (LRRs) are predicted by comparison with known proteins and by the presence of the core sequence: $xxxFxxLxxLxxLxLxxNxIxxL$, where x is any amino acid. In slit proteins, the LRRs are flanked by conserved sequences referred to as the amino- and carboxy- flanking regions. These flanking regions are found in other known proteins, but only in a few instances are both the amino- and carboxy- flank regions present in a single protein. The amino flank region is defined by the consensus: $CPxxCx[1-6x]GxxVDCxxxGL[2-4x]\alpha Pxx\alpha Pxdttx$ where x is any amino acid, $[x]$ represents a variable number of amino acids and α is a hydrophobic residue. Lower case indicates a residue is not highly conserved at a particular position. The carboxy flank region is defined by the consensus: $P\beta xC\gamma Cx\alpha[1-5x]W\alpha[14-26x]RCxxPxxxxxxxx\alpha xx\alpha xxxxF[1-3x]Cs[3-17x]$ where β is W or a hydrophobic residue, γ is D or N and α is a hydrophobic residue.

Epidermal growth factor (EGF) repeats are predicted by the consensus: $CxxxxCxngxC[6-9x]\alpha xCxCxG\alpha xGxxCxxxxxx$.

The so called "99aa spacer" is actually ~200 amino acids in the Drosophila protein and 174 amino acids in Human Slit-1. This region shows homology to the G-loops of laminin A chains.

Cysteine knots are dimerisation domains defined by the presence of six cysteine residues between which disulphide bridges form. The only absolutely conserved residues are the six cysteines, and spacing between them is highly variable, apart from between cysteines 2 and 3, and 5 and 6: C[x]C[1-3x]GxC[x]C[x]CxC. The glycine between cysteines 2 and 3 is only present in a subset of cysteine knots. Drosophila slit and Human slit-1 both have an extra cysteine after cysteines 5 and 6: this may serve as an intermolecular bond.

Human Slit-1 gene displays the overall structure of the Drosophila gene, and amino acid conservation is found along the entire length of the protein (48% homology at the amino acid sequence excluding the signal sequence; see below). The Human gene has an extra LRR between LRR2 and LRR3 of the first set of LRRs; in the third set, the Human gene has an extra LRR between LRR3 and LRR4. The Human gene has two extra EGF repeats, on either side of the seventh EGF repeat in Drosophila slit.

Isolation of Human slit-1

Searching of the EST database revealed an EST, ab16g10.r1, with homology to the 99aa spacer region of Drosophila slit. This EST was used to probe a Human fetal brain library (Stratagene), and clones for Human slit-1 were isolated.

100% 95% 90% 85% 80%

Amino acid identity between Drosophila Slit and Human Slit-1

First amino-flanking sequence:	53%
First set of Leucine Rich Repeats:	52% (54%, 67%, NA, 38%, 54%, 50%)
First carboxy-flanking sequence:	42%
Second amino-flanking sequence:	50%
Second set of Leucine Rich Repeats:	60% (54%, 58%, 67%, 71%, 50%)
Second carboxy-flanking sequence:	62%
Third amino-flanking sequence:	56%
Third set of Leucine Rich Repeats:	49% (46%, 46%, 42%, NA, 58%)
Third carboxy-flanking sequence:	36%
Fourth amino-flanking sequence:	53%
Fourth set of Leucine Rich Repeats:	48% (25%, 58%, 46%, 63%)
Fourth carboxy-flanking sequence:	63%
First EGF repeat:	34%
Second EGF repeat:	46%
Third EGF repeat:	46%
Fourth EGF repeat:	35%
Fifth EGF repeat:	47%
Spacer:	22%
Sixth EGF repeat:	40%
"99aa spacer":	38%
Seventh EGF repeat:	11%/NA
Eighth EGF repeat:	44%
Nineth EGF repeat:	29%/NA
Cysteine knot motif:	34%

NA: not applicable due to absence of homologous repeat.

Figures for individual LRRs are shown in brackets.

TABLE 3

Alignment of

Slit sequences

1	M A A P S R T T L M P P P F R L Q L R L - L I L P I I L L L R H D A V H A E P Y	D-Slit
1	M R G V G W Q - - - - M L S L S L G L V L A I L - - - - -	H-Slit1
40	S G G F G S S A V S S G G L G S V G I H I P G G G V G V I T E A R C P R V C S C	D-Slit
21	- - - - - - - - - - N K V A P Q A C P A Q C S C	H-Slit1
80	T G L N V D C S H R G L T S V P R K I S A D V E R L E L Q G N N L T V I Y E T D	D-Slit
35	S G S T V D C H G L A L R S V P R N I P R N T E R L D L N G N N I T R I T K T D	H-Slit1
120	F Q R L T K L R M L Q L T D N Q I H T I E R N S F Q D L V S L E R L - - - - -	D-Slit
75	F A G L R H L R V L Q L M E N K I S T I E R G A F Q D L K E L E R L R L N R N H	H-Slit1
1	H L R V L Q L M E N R I S T I E R G A F Q D L K E L E R L R L N R N N	M-Slit1
154	- - - - - - - - - - D I S N N V I T T V G R R V F K G A Q S L R	D-Slit
115	L Q L F P E L L F L G T A K L Y R L D L S E N Q I Q A I P R K A F R G A V D I K	H-Slit1
36	L Q L F P E L L F L G T A R L Y R L D L S E N Q I Q A I P R K A F R G A V D I K	M-Slit1
176	S L Q L D N N Q I T C L D E H A F K G L V E L E I L T L N N N N L T S L P H N I	D-Slit
155	N L Q L D Y N Q I S C I E D G A F R A L R D L E V L T L N N N N I T R L S V A S	H-Slit1
76	N L Q L D Y N Q I S C I E D G A F R A L R D L E V L T L N N N N I T R L S V A S	M-Slit1
216	F G G L G R L R A L R L S D N P F A C D C H L S W L S R F L R S A T R L A P Y T	D-Slit
195	F N H M P K L R T F R L H S N N N L Y C D C H L A W L S D W L R K R P R V G L Y T	H-Slit1
116	F N H M P K L R T F R L H S N N N L Y C	M-Slit1
256	R C Q S P S Q L K G Q N V A D L H D Q E F K C S G L T E - H A P M - - - E C G A	D-Slit
235	Q C M G P S H I L R G H N V A E V Q K R E F V C S D E E E G H Q S F M A P S C S V	H-Slit1
292	E N S C P H P C R C A D G I V D C R E K S L T S V P V T L P D D T T D V R L E Q	D-Slit
275	L H - C P A A C T C S N N I V D C R G K G L T E I P T N L P E T I T E I R L E Q	H-Slit1
12	S P C T C S N N I V D C R G K G L M E I P A N L P E G I V E I R L E Q	H-Slit2
352	N F I T E L I P P K S F S S F R R L R R I D L S N N N I S R I A H D A L S G L K Q	D-Slit
314	N T I K V I P P P G A F S P Y K K L R R I D L S N N N Q I S E L A P D A F Q G L R S	H-Slit1
36	N S I K A I P A G A F T Q Y K K L K R I D I S K N O I S D I A P D A F Q G L K S	H-Slit2
372	L T T L V L Y G N K I K D L P S G V F K G L G S L R L L L N A N E I S C I R K	D-Slit
354	L N S L V L Y G N K I T E L P K S L F E G L F S L Q L L L N A N K I N C L R V	H-Slit1
76	L T S L V L Y G N K I T E I A K G L F D G L V S L Q L L L	H-Slit2
1	D A F R D L H S L S L L S L Y D N N I Q S L A N G T F D A M K S M K T V H L A K R	CE-Slit
412	D A F Q D L H N L N L L S L Y D N K L Q T I A K G T F S P L R A I Q T M H L A Q	D-Slit-
394		H-Slit1
2	N P X I C D C N L Q W L A Q I N L Q K N I E T S G A R C E Q P K R L R K K K F A	CE-Slit
452	N P F I C D C N L R W L A D Y L H K N P I E T S G A R C E S P K R M H R R R I E	D-Slit
434	N P F I C D C H L K W L A D Y L H T N P I E T S G A R C T S P R R L A N K R I G	H-Slit1
42	T L P P N K F K C K G S E S F V S M Y A D S C F I D S I C P T Q C D C Y G T T V	CE-Slit
492	S L R E E K F K C S - W G E L R M K L S G E C R M D S D C P A M C H C E G T T V	D-Slit
474	Q I K S K K F R C S G T E D Y R S K L S G D C F A D L A C P E K C R C E G T T V	H-Slit1

82 D C N K R G L N T I P T S I P R F A T Q L L L S G N N I S T V D L N S N I H V L CE-Slit
 531 D C T G R R L K E I P R D I P L H T T E L L L N D N E L G R I S S D G L F G R L D-Slit
 514 D C S N Q K L N K I P E H I P Q Y T A E L R L N N N E F T V L E A T G I F K K L H-Slit1

122 E N L E X L D L S N N H I T F I N D K S F E K L S K L R E L X L N D CE-Slit
 571 P H L V K L E L K R N Q L T G I E P N A F E G A S H I Q E L Q L G E N K I K E I D-Slit
 554 P Q L R K I N F S N N K I T D I E E G A F E G A S G V N E I L L T S N R L E N V H-Slit1
 1 E G A F N G A A S V O E L M L T G H Q L E T V H-Slit2

611 S N K M F - L G L H Q L K T L N D-Slit
 594 Q H K M F K G - L E S L K T L M L R S N R I T C V G N D S F I G L S S V R L L S H-Slit1
 24 H G R G F R G G L S G L K T L M L R S N L I G C V S N D T F A G L S S V R L L S H-Slit2

626 L Y D N Q I S C V M P G S F E H L N S L T S L N L A S N P F N C N C H L A W - F D-Slit
 633 L Y D N Q I T T V A P G A F D T L H S L S T L N L L A N P F N C N C Y L A W - L H-Slit1
 64 L Y D N R I T T I T P G A F T T L V S L S T I N L L S N P F N C N C H L G A G L H-Slit2

665 A E C V R K K S L N G G A A R C G A P S K V R D V Q I K D L P H S E F K C S S E D-Slit
 672 G E W L R K K R I V T G N P R C Q K P Y F L K E I P I Q D V A I Q D F T C D D G H-Slit1
 104 G K W L R K R R I V S G N P R C Q K P F F L K E I P I Q G V G H P G I H-Slit2

1 N S E - G C L G D G Y C P P S C T C T G T V V A C S R N Q L K E I P R G I P A E CE-Slit
 705 H D D N S C S P L S R C P T E C T C L D T V V R C S N K G L K V L P K G I P R D D-Slit
 712 H-Slit1

16 T T E L Y L D A N Y I N E I P A H D I N R L Y S L T K L D D L S H N R L I S L E N CE-Slit
 744 T S E L Y L E S N E I E Q I H Y E R I R H L R S L T R L D D L S N N Q I T I L S N D-Slit
 732 V T E L Y L D G N Q F T L V P K E - L S N Y K H L T L I D L S N N R I S T L S N H-Slit1

56 N T F S N L T R L S T L I I S Y N K L R C L Q P L A F N G L N A L R I I L S L H G CE-Slit
 784 Y T F A N L T K L S T L I I S Y N K L Q C L Q R H A L S G L N N L R V V S L H G D-Slit
 791 Q S F S N M T Q L L T L I L S Y N R L R C I P P R T F D G L K S L R L L S L H G H-Slit1

96 N D I S F L P Q S A F S N L T S I T H I A V G S N S L Y C D C N M A W F S K W I CE-Slit
 824 N R I S M L P E G S F E D L K S L T H I A L G S N P L Y C D C G L K W F S D W I D-Slit
 831 N D I S V V P E G A F N D L S A L S H L A I G A N P L Y C D C N M Q W L S D W V H-Slit1

136 K S K F I E A G I A R C E Y P N T V S N Q L L T A Q P Y Q F T C D S K V P T K CE-Slit
 864 K L D Y V E P G I A R C A E P E Q M K D K L I L S T P S S S F V C R G R V R N D D-Slit
 871 K S E Y K E P G I A R C A G P G E M A D K L L T T P S K K F T C Q G P V D V N H-Slit1

176 L A T K C D L C L N S P C K N N A I C E T T S S R K Y T C N C T P G F Y G V H C CE-Slit
 904 I L A K C N A C F E Q P C Q N Q A Q C V A L P Q R E Y Q C L C Q P G Y H G K H C D-Slit
 911 I L A K C N P C L S N P C K N D G T C N S D P V D F Y R C T C P Y G F K G Q D C H-Slit1

216 E N Q I D A C Y G S P C L N N A T C K V - - A Q A G R F N C Y C N K G F E G D Y CE-Slit
 944 E F M I D A C Y G N P C R N N A T C T V L E - - E G R F S C Q C A P G Y T G A R D-Slit
 951 D V P I H A C I S N P C K H G G T C H L K E G E E D G F W C I C A D G F E G E N H-Slit1

254 C E K N I D D C V - N S K C E N G G K C V D L V R F C S E E L K N F Q S F Q I N CE-Slit
 982 C E T N I D D C L G E I K C Q N N A T C I D - - - - - - - - - - - - - - - - G V E D-Slit
 991 C E V N V D D C - E D N D C E N N S T C V D - - - - - - - - - - - - - - - - G I N H-Slit1

293 S Y R C D C P M E Y E G K H C E D K L E Y C T K K L N P C E N N G K C I P I N G
 1007 S Y K C E C Q P G F S G E F C D T K I Q F C S P E F N P C A N G A K C M D H F T
 1015 N Y T C L C P P E Y T G E L C E E K L D F C A Q D L N P C Q H D S K C I L T P K
 1 D P L P V
 CE-Slit
 D-Slit
 H-Slit1
 M-Slit2

333 S Y S C M C S P G F I T G N N C E T N I D D C K N V E C Q N G G S C V D G I L S Y
 1047 H Y S C D C Q A G F H G T N C T D N I D D C Q N H M C O N G G T C V D G I N D Y
 1055 G F K C D C T P G Y V G E H C D I D F D D C Q D N K C K N G A A C T D A V N G Y
 1 N N D D C V G H K C R H G A Q C V D E V N G Y
 1 W P R C E C M P G Y A G D N C S E N Q D D C R D H R C Q N G A Q C M D E V N S Y
 6 H H R C E C M L G Y T G D N C S E N O D D C K D H K C Q N G A Q C V D E V N S Y
 M-Slit1
 H-Slit2
 M-Slit2

373 D C L C R P G Y A G Q O Y C E I P P M M D M E Y Q K T D A C Q Q S A C G Q G - E C
 1087 Q C R C P D D Y T G K Y C E G H N M I S M M Y P Q T S P C Q N H E C K H G V - C
 1095 T C I C P E G Y S G L F C E F S P - - P M V L P R T S P C D N F D C Q N G A Q C
 24 T C I C P Q G F S G L F C E H P P - - P M V L L Q T S P C D Q Y E C Q N G A Q C
 41 S C L C A E G Y S G Q L C E I P P - - H L P A P K - S P C E G T E C Q N G A N C
 46 A C L C V E G Y S G Q L C E I P P - - - - A P R - S S C E G T E C Q N G A N C
 M-Slit1
 H-Slit2
 M-Slit2

412 V A S Q N - S S D F T C K C H E G F S G P S C D R Q M S V G F K N P G A Y L A L
 1126 F Q P N A Q G S D Y L C R C H P G Y T G K W C E Y L T S I S F V H N N S F V E L
 1133 I V R I N E P - - - I C Q C L P G Y Q G E K C E K L V S V N F I N K E S Y L Q I
 62 I V V Q Q E P - - - T C R C P P G F A G P R C E K L I T V N F V G K D S Y V E L
 78 V D Q G N R P - - - V C Q C L P G F G G P E C E K L L S V N F V D R D T Y L Q F
 80 V D Q G S R P - - - V C Q C L P G F G G P E C E K L L S V N F V D R D T Y L Q F
 M-Slit1
 H-Slit1
 M-Slit1
 H-Slit2
 M-Slit2

451 D P L A S - - D G T I T M T L R T T S K I G I L L Y Y G D D H F V S A E L Y D G
 1166 E P L R T R P E A N V T I V F S S A E Q N G I L M Y D G Q D A H L A V E L F N G
 1170 P S A K V R P Q T N I T L Q I A T D E D S G I L L Y K G D K D H I A V E L Y R G
 99 A S A K V R
 115 T D L Q N W X R X N I T L Q V F T A E D N G I L L Y N G G N D H I A V X L Y X G
 117 T D L Q N W P R A N I T L Q V S T A E D N G I L L Y N G D N D H I A V E L Y
 M-Slit1
 H-Slit2
 M-Slit2

489 R V K L V Y Y I G N F P A S H H M Y S S V K V N D G L P H R I S I R T S E R K C F
 1206 R I R V S Y D V G N H P V S T H M Y S F E M V A D G K Y H A V E L L A I K K N F T
 1210 R V R A S Y D T G S H P A S A I Y S V E T I N D G N F H I V E L L A L D Q S L S
 155 H V R F S Y
 CE-Slit
 D-Slit
 H-Slit1
 M-Slit2

529 L Q I D K N P V Q I V E N S G K S D Q L I T K G K E M L Y I G G L P I E K S Q D
 1246 L R V D R G L A R S I I N E G S N D Y L - - K L T T P M F L G G L P V D P A Q Q
 1250 L S V D G G N E K I I T N L S K Q S T L - - N F D S P L Y V G G M P G K S N V A
 1 I L D V A
 CE-Slit
 D-Slit
 H-Slit1
 M-Slit1

569 A K R R F H V K N S E S L K G C I S S I T I N E V P I N L Q Q A L E N V N T E Q
 1284 A Y K N W Q I R N L T S F K G C M K E V W I N H K L V D F G N A Q R Q Q K I T P
 1288 S L R Q A P G Q N G T S F H G C I R N L Y I N S E L Q D F Q K V P M Q T G I L P
 6 S L R Q A P G E N G T S F H G C I R N L Y I N S E L Q D F R K M P M O T G I L P
 CE-Slit
 D-Slit
 H-Slit1
 M-Slit1

609 S C - - - - - - - - S A T V N F - - - - - - - -
 1324 G C A L - - - L E G E Q Q E E D D E Q D F M D E - - - - T P H I K E E P
 1328 G C E P C H K K V C A H G T C Q P P S S Q A G F T C E C Q E G W M G P L C D Q R T
 46 G C E P C H K K V C A H G C C Q P S S Q S G F T C E C E E G W M G P L C D Q R T
 CE-Slit
 D-Slit
 H-Slit1
 M-Slit1

617	- - - C A C I D C G N G - K C T N N A L S P K G Y M C O C D S H F S G E H C D E	CE-Slit
1354	V D P C L E N K C R R G S R C V P N S N A R D G Y Q C K C K H G Q R G R Y C D Q	D-Slit
1368	X D P C L G N K C V H G T - C L P I N A F - - S Y S C K C L E G H G G V L C D E	H-Slit1
86	X D P C L G N K C V H G T - C L P I N A F - - S Y S C K C L E G H G G V L C D E	M-Slit1
653	- -	
1394	G E G S T E P -	CE-Slit
1405	E E D L F N P C Q A I K C K H G K C R L S G L G Q P Y C E C S S G Y T G D S C D	D-Slit
123	C F D L F N P C Q M A I K C K H G K C R L S G V G Q P Y C E C N S G F T G D S C D	H-Slit1
1	Q C H I S D Q G E P Y C L C Q P G F S G E H C Q	M-Slit1
1	A F K C H H G O C H T S D R G E P Y C L C Q P G F S G H H C E	H-Slit2
653	K R I K C D K Q K F R R H H I E N E - - - - - C R S V D R I K I A E C N G Y C G G	CE-Slit
1408	T - - - C R K E Q V R E Y Y T E N D - - - - - C R S R O P L K Y A K C V G G C G -	D-Slit
1445	R E I S C R G E R I R D Y Y Q K Q Q G Y A A C Q T T K K V S R L E C R G G C A G	H-Slit1
163	R E I S C R G E R I R D Y Y Q K Q Q G Y A A C Q T T K K V S R L E C R G G C A G	M-Slit1
25	Q E N P C L G Q V V R E V I R R Q K G Y A S C A T A S K V P I M E C R G G C - G	H-Slit2
32	Q E N P C M G E I V R E A I R R O K D Y A S C A T A S K V P I M E C R G G C - G	M-Slit2
689	E O N C C T A V K K * Q R K V K M I C K N G T T K I S T V H I I R Q C Q C E P T	CE-Slit
1440	- N Q C C A A K I V R R R K V R N V C S N N R K Y I K N L D I V R K C G C - - T	D-Slit
1485	G Q - C C G P L R S K R R K Y S F E C T D G S S F V D E V E K V V K C G C T R -	H-Slit1
203	G Q - C C G P L R S K R R K Y S F E C T D G S S F V D E V E K V V K C G C A R -	M-Slit1
64	P Q - C C Q P T R S K R R K Y V F Q C T D G S S F V E E V E R H L E C G C L A -	H-Slit2
71	T T - C C Q P I R S K R R K Y V E Q C T D G S S F V E E V E R H L E C G C R A -	M-Slit2
729	R S V L S E K	CE-Slit
1477	R K C Y	D-Slit
1523	- - C V S	H-Slit1
241	- - C A S	M-Slit1
102	- - C - S	H-Slit2
109	- - C - S	M-Slit2

TABLE 4

Alignment of Drosophila Slit and Human Slit-1

1 MAAPSRTTLMPPPFRLQLRL-LILPILLLLRHDAVHAEPY D-Slit
 1 MRGVGWQ-----MLSLSLGLVLAILE----- H-Slit1
 40 SGGFGSASVSSGGGLGSVGIGHIPGGGVGVITEARCPRVCS C
 21 -----NKVAPQACPAQCSC D-Slit
 H-Slit1
 80 TGLNVDCSHRGLTSPVRKISADVERLELQGNNLTVIYE TD
 35 SGSTVDCHGLALRSVPRNIPRNTERLDLNGNNITRITKT D-Slit
 H-Slit1
 120 FQRLTKLRLMLQLTDNQIHHTIERNSFQDLVSLERL D-Slit
 75 FAGLRLRVLQLOLMEHKISTIERGAFQDLKELERLRLRNHN H-Slit1
 154 -----DISNNVITTVGRRVFKGAQS L R D-Slit
 115 LQLFPPELLFLGTAKLYRLDLSENQIQAI PRKAFRGAVD I K H-Slit1
 176 SLQLDDNNQITCLDEHAFKGLVELEILT L N N N N L T S L P H N I D-Slit
 155 NLQOLDYNOIISCIEDGAFRALRDLEVLTLNNNNITRLSVA S H-Slit1
 216 FGGLGRLRALRLSDNPFA C D C H L SWLSRF L RSATR LAP Y T D-Slit
 195 FNHMPKLRTRFLHSNNLYC D C H L A W L S D W L R K R P R V G L Y T H-Slit1
 256 RCQSPSQQLKGQNVADLHDQE FKCSGLTE-HAPM---ECGA D-Slit
 235 QCMGPSPHLRGHNVAEVQKREFVCSDEEEGHQSFMAPS CGSV H-Slit1
 292 ENSCPHPCCRCAADGIIVDCREKSLTSVPVTLPDDTTDVRL EQ D-Slit
 275 LH-CPAACTCSNNIVDCRGKGLTEIPTNLPEТИEIRLEQ H-Slit1
 332 NFITELPPKSFS SFRRLRRIDLSSNNNISRIAHDALSGLKQ D-Slit
 314 NTIKVIPPAGAFSPYKKLRRIDLSSNNQISELAPDAFQGLRS H-Slit1
 372 LTTLVLYGNKI KDLPSGSVFKGLGSLRLLLNNANEIISCIRK D-Slit
 354 LNSLVLVLYGNKITEELPKSLEEGLFSLQLLLNNANKINCLRV H-Slit1
 412 DAFRDLDHSLSLSSLYDNNNIQSLANGTFDAMKSMKTVHLAK D-Slit
 394 DAFQDLHNNLNLSSLYDNKLQTIAKGTFSPRLAIQTMHLAQ H-Slit1
 452 NPFIICDCNLRWLADYLHKNPPIETSGARCESPDKRMHRRRIE D-Slit
 434 NPFIICDCHLKWLADYLHTNPPIETSGARCTS P R R L A N K R I G H-Slit1
 492 SLREEEKFKCS-WGELRMRMKLSGECRMDSDCPAMCHCEGTTV D-Slit
 474 QIKSKKFKCSGTEDYRSKLSGDCAFADLACPEKCRCEGTTV H-Slit1
 531 DCTGRRRLKEIPRDIPLHTTELLLNDNELGRISSDGLFGRL D-Slit
 514 DCASNQQLNKPipeHIPOQYTAELRLNNNEFTVLEATGIFKKL H-Slit1
 571 PHLVKLELKRNQLTGTIEPNAFEGASHIQELQLGENKIKEI D-Slit
 554 PQQLRKINFSSNNKITDIEEGAFEGASGVNEILLTSNRLENV H-Slit1
 611 SNKMFGLHQQLKTL----- N L D-Slit
 594 QHKMFKGLESLKTLMLRSNRITCVGNDSFIGLSSVRLLSL H-Slit1
 627 YDNQISCVMPGGSFEHLNSLTSLNLASNPFCNCCHLAWFAE D-Slit
 634 YDNOITTVAPGAFDTLHSSLSTLNLLANPFNCNCYLAWLGE H-Slit1

667 C V R K K S L N G G A A R Q A P S K V R D V Q I K D L P H S K C S S E N S D-Slit
 674 W L R K K R I V T G N P R C Q K P Y F L K E I P I Q D V A I Q D Y T C D D G N D H-Slit1

707 E - G C L G D G Y C P P S C T C T G T V V A C S R N Q L K E I P R G I P A E T S D-Slit
 714 D N S C S P L S R C P T E C T C L D T V V R C S N K G L K V L P K G I P R D V T H-Slit1

746 E L Y L E S N E I E Q I H Y E R I R H L R S L T R L D L S N N Q I T I L S N Y T D-Slit
 754 E L Y L D G N Q F T L V P K E - L S N Y K H L T L I D L S N N R I S T L S M Q S H-Slit1

786 F A N L T K L S T L I I S Y N K L Q C L Q R H A L S G L N N L R V V S L H G N R D-Slit
 793 F S N M T Q L L T L I L S Y N R L R C I P P R T F D G L K S L R L L S L H G N D H-Slit1

826 I S M L P E G S F E D L K S L T H I A L G S N P L Y C D C G L K W F S D W I K L D-Slit
 833 I S V V P E G A F N D L S A L S H L A I G A N P L Y C D C N M Q W L S D W V K S H-Slit1

866 D Y V E P G I A R C A E P E Q H K D K L I L S T P S S S F V C R G R V R N D I L D-Slit
 873 E Y K E P G I A R C A G P G E H A D K L L L T T P S K K F T C Q G P V D V N I L H-Slit1

906 A K C N A C F E Q P C Q N Q A Q C V A L P Q R E Y Q C L C Q P G Y H G K H C E F D-Slit
 913 A K C N P C L S N P C K H D G T C N S D P V D F Y R C T C P Y G F K G Q D C D V H-Slit1

946 M I D A C Y G N P C R N N A T C T V L E - - E G R F S C Q C A P G Y T G A R C E D-Slit
 953 P I H A C I S N P C K H G G T C H L K E G E E D G F W C I C A D G F E G E N C E H-Slit1

984 T H I D D C L G E I K C Q H H A T C I D G V E S Y K C E C Q P G F S G E F C D T D-Slit
 993 V H V D D C - E D N D C E H U S T C V D G I N N Y T C L C P P E Y T G E L C E E H-Slit1

1024 K I Q F C S P E F H P C A N G A K C M D H F T H Y S C D C Q A G F H G T N C T D D-Slit
 1032 K L D F C A Q D L N P C Q H D S K C I L T E K G F K C D C T P G Y V G E H C D I H-Slit1

1064 N I D D C Q N H M C Q N G G T C V D G I N D Y Q C R C P D D Y T G K Y C E G H N D-Slit
 1072 D F D D C Q D N K C K N G A H C T D A V H G Y T C I C P E G Y S G L F C E F S P H-Slit1

1104 M I S H M Y P Q T S P C Q H E C K H G V - C F Q P N A Q G S D Y L C R C H P G D-Slit
 1112 - - P M V L P R T S P C D N F D C Q N G A Q C I - - V R I N E P I C Q C L P G H-Slit1

1143 Y T G K W C E Y L T S I S F V H N N S F V E L E P L R T R P E A H V T I V F S S D-Slit
 1147 Y Q G E K C E K L V S V N F T I N K E S Y L Q I P S A K V R P Q T H I T L Q I A T H-Slit1

1183 A E Q N G I L M Y D G Q D A H L A V E L F N G R I R V S Y D V G N H P V S T M Y D-Slit
 1187 D E D S G I L L Y K G D K D H I A V E L Y R G R V R A S Y D T G S H P A S A I Y H-Slit1

1223 S F E M V A D G K Y H A V E L L A I K K N F T L R V D R G L A R S I I N E G S N D-Slit
 1227 S V E T I N D G N F H I V E L L A L D Q S L S I S V D G G N P K I I T M L S K Q H-Slit1

1263 D Y L K L T T P M F L G G L P V D P A Q Q A Y K N W Q I R N L T S F K G C M K E D-Slit
 1267 S T L N F D S P L Y V G G M P G K S N V A S L R Q A P G Q N G T S F H G C I R N H-Slit1

1303 V W I N H K L V D F G N A Q R Q Q K I T P G C A L - - - L E G E Q Q E E E D D D-Slit
 1307 L Y I N S E L Q D F Q K V P M O T G I L P G C E P C H K K V C A H G T C Q P S S H-Slit1

1339 E Q D F M D E - - - - T P H I K E E P V D P C L E N K C R R G S R C V P N S D-Slit
 1347 Q A G F T C E C Q E G W M G P L C D Q R T N D P C L G N K C V H G T - C L P I N H-Slit1

1373 N A R D G Y Q C K C K H G Q S R Y C D Q G E G S T E P - - - - -
1386 A F - - S Y S C K C L E G H G G V L C D E E E D L F N P C Q A I K C K H G K C R D-Slit
H-Slit1

1401 - - - - - P T V T A A S - - - T C R K E Q V R E Y Y T E N D - D-Slit
1424 L S G L G Q P Y C E C S S G Y T G D S C D R E I S C R G E R I R D Y Y Q K Q Q G H-Slit1

1423 - - - C R S R Q P L K Y A K C V G G C - G N Q C C A A K I V R R R K V R M V C S D-Slit
1464 Y A A C Q T T K K V S R L E C R G G C A G G O C C G P L R S K R R K Y S F E C T H-Slit1

1459 N N R K Y I K N L D I V R K C G C T K K C Y
1504 D G S S F V D E V E K V V K C G C T R - C V S D-Slit
H-Slit1

2007-06-15 14:20:44 2007-06-15 14:20:44

TABLE S(A)

Hybridisation Probes for regions of Human Slit-1

Hybridisation Probe for the first Leucine rich repeat region

TGCCCCGGCGCAGTGCCTTGCTCGGGCAGCACAGTGGACTGTCACGGGCTGGCGCTGCCAGCGTGCCAGGAAT	75
ATCCCCCGAACACCGAGAGACTGGATTAAATGGAATAACATCACAAAGAATTACGAAGACAGATTGGCTGGT	150
CTTAGACATCTAAGAGTTCTCAGTTATGGAGAATAAGATTAGCACCATTGAAAGAGGAGCATGCCAGGATCTT	225
AAAGAACTAGAGAGACTGGTTAACAGAAATCACCTCAGCTGTTCTGAGTTGCTGTTCTGGGACTGCG	300
AAGCTATACAGGCTGATCTCAGTAAAACCAATTAGGAAATCCCAGGAAAGCTTCCGTGGGAGCTGAC	375
ATAAAAAAATTGCAACTGGATTACAACCAGATCAGCTGATTGAAGATGGGCAATTCAAGGATCTCCGGGACCTG	450
GAAGTGCTCACTCTAACAAACATTAGACTTCTGTCAGTAAACCTGGGCTCTCCGACTGGCTTCGAAAGG	525
ACTTTTCGACTGCATTCAAACACCTGTATTGTGACTGCCACCTGGGCTCTCCGACTGGCTTCGAAAGG	600
CCTCGGGTTGGTCTGTACACTCAGTGTATGGGCCCCCTCCACCTGAGAGGCCATAATGTAGCCGAGGTTCAAAA	675
CGAGAATTGCTGCAGTGATGAGGAAGAGTCACCAAGTCATTATGGCTCTTCTGTAGTGTGAC	747

82 - 828

Hybridisation Probe for the second Leucine rich repeat region

TGCCCTGCCGCTGTACCTGTAGCAACAATATCGTAGACTGTCGTGAAAGGTCTACTGAGATCCCCACAAAT	75
CTTCCAGAGACCATCACAGAAATACGTTGGAACAGAACACAATCAAAGTCATCCCTCTGGAGCTTCTCACCA	150
TATAAAAAGCTTAGACGAATTGACCTGAGCAATAATCAGATCTGAACTTGCACCAAGATGCTTCCAAGGACTA	225
CGCTCTCTGAATTCACTTGTCTCTATGGAATAAAATCACAGAACACTCCCCAAAGTTATTGAAGGACTGTT	300
TCCTTACAGCTCCTATTATTGAATGCCAACAGATAAACTGCTTCTGGTAGATGCTTTCAGGATCTCCACAAAC	375
TTGAACCTCTCTCCCTATATGACAACAAGCTCAGACCCTGCCAAGGGACCTTTCACCTCTCGGGCATT	450
CAAACATGCATTGGCCAGAACCCCTTAATTGTGAATGCCATCTCAAGTGGTAGCGGATTATCTCCATACC	525
AACCCGATTGAGACCAGTGGTCCCCGTTGACAGGCCCGCCGCTGGCAAACAAAAGAATTGGACAGATCAAAC	600
AGCAAGAAATTCCGTTGTCAGGTACAGAACATTGATCAAATTAAGTGGAGACTGCTTGGGATCTGGCT	675

829 - 1503

Hybridisation Probe for the third Leucine rich repeat region

TGCCCTGAAAAGTGTGCGTGTGAAGGAACACAGTAGATTGCTCTAACAAAGCTAACAAATCCGGAGCAC	75
ATTCCCCAGTACACTGCAGAGTTGCGTCATAATAATGAATTACCGTGTGGAGGCCACAGGAATCTTAAAG	150
AAACTTCTCAATTACGAAATAAAACTTTAGCAACAATAAGATCACAGATAATTGAGGAGGGAGCATTTGAAGGA	225
GCATCTGGTGAATGAAATACTTCTTACGAGTAATCGTTGAAAATGTGAGCATAAGATGTTCAAGGGATTG	300
GAAAGCCTCAAAACTTGTGATGTTGAAAGCAATCGAATAACCTGTGTGGGAATGACAGTTCATAGGACTCAGT	375
TCTGTGCGTTGTTCTTGTATGATAATCAAATTACTACAGTTGCACCAAGGGCATTGATACTCTCCATTCT	450
TTATCTACTCTAAACCTCTGGCAATCCTTTAATGTAACGTACCTGGCTGGTTGGAGAGTGGCTGAGA	525
AAGAAGAGAAATTGTACGGGAATCTAGATGTCAAAACCATACTTCTGAAAGAAATACCCATCCAGGATGTG	600
GCCATTCAAGGACTTCAATTGATGACGGAAATGATGACAATAGTGTGCTCCCACTTCTCGC	663

1504 - 2166

Hybridisation Probe for the fourth Leucine rich repeat region

TGTCTACTGAATGTAATTGCTGGATACAGTCGTCGATGTAGCAACAAGGGTTGAAGGTCTTGGCAGAGGT	75
ATTCCAAGAGATGTACAGAGTTGTATCTGGATGAAACCAATTACACTGGTCCCAAGGAACCTCCAACTAC	150
AAACATTAAACACTTATAGACTTAAGTAACAAACAGAATAAGCACGCTTCTAACATCAGAGCTTCAGCAACATGACC	225
CAGCTCTCACCTTAATTCTTAGTTACAACCGCTGAGATGTTACCTCTCGCACCTTGATGGATTAAAGTCT	300
CTTCGATTACTTCTCTACATGGAAATGACATTCTGTTGCTGAGGTGCTTCAATGATCTTCTGCATTA	375
TCACATCTAGCAATTGGAGCCAACCCCTTTACTGTGATTGTAACATGCAGTGGTATCCGACTGGTGAAGTGG	450
GAATATAAGGAGCTGGATTGCTCGTGTGCTGGCCTGGAGAAATGGCAGATAAAACTTTACTCACAACTCCC	525
TCCAAAAAAATTACCTGTCAAGGTCTGTGGATGTCAATTACTAGTCAAGTGTAAACCC	585

2167 - 2171

Hybridisation Probe for EGF repeats one to five

TGCCATCAATCCGTGAAAAATGATGGCACATGTAATAGTGTACCTTACCGATGCACCTGTCCA	75
TATGGTTCAAGGGCAGGACTGTGATGTCCTAACATTGATGCCATCAGTAACCCATGTAACATGGAGGAAC	150
TGCCACTTAAAGGAAGGAGAAAGATGATGGATTCTGGTGTATTGTGCTGATGGATTGAGGAGAAAATTGTGAA	225
GTCAACGTTGATGATTGAAAGATAATGACTGTGAAATAATTCTACATGTGTCGATGGCATTAAATAACTACACA	300
TGCCCTTGCCCCACCTGACTTACAGGTGAGTTGAGGAGAAGCTGGACTCTGTGCTGGCAGGACCTGAACCCC	375
TGCCAGCACGATTCAAAGTGCATCCTAACCTCCAAAGGGATTCAAATGTGACTGCACACCAGGGTACGTAGGTGAA	450
CACTGCGACATCGATTGACGACTGCCAACACAAGTGTAAAACGGAGGCCACTGCACAGATGCAGTGAAC	525
GGCTATACGTGCATATGCCCGAAGGTTACAGTGGCTGTTCTGTGAGTT	576

2168 - 2172

TABLE 5(B)

Hybridisation Probe for the sixth EGF repeat and preceding spacer region

TCTCCACCCATGGCTTCCCTGTCAGGCCCTGTGATAATTITGATTGTCAGAATGGAGCTAGTGATCGTC
AGAATAAAATGAGCCCATATGTCAGTGTTCGCTGGCTATCAGGGAGAAAAGTGTGAAAA

75
134

3:28 - 3:41

Hybridisation Probe for the 99aa spacer/G-loop region

ATTGGITAGTGTGAATTATAACAAAGAGTCTTATCTTCAGATTCCAGGCCAAGGTTCGGGCTCAGACCAA
CATAACACTTCAGATTGCCACAGATGAAGACAGCGGAATCTCCTGTATAAGGTTGACAAGACCATA
AGAACTCTATCGGGGCGTGTCTGCCAGCTATGACACCGGCTCTCATCCAGCTTGTGCCATTACAGTGTGGA
GACAATCAATGATGAAACTTCCACATTGTGGAACACTATTGCCTGGATCAGAGTCTCTCTTGTCCGTGGATGG
TGGGAACCCCCAAAATCATCACTAACTTGTCAAAGCAGTCCACTCTGAATTGACTCTCCACTCTATGTAGGAGG
CATGCCAGGGAAAGACTAACGTGGCATCTCTGCCAGGCCCTGGGCGAACCGGAAACAGCTTCCACGGCTGCAT
CCGGAACCTTACATCAACAGTGAGCTGCAGGACTTCCAGAAGGTGCGATGCAAACAGGCATTGTGGCTGT

75
150
225
300
375
450
526

1162 - 3987

Hybridisation Probe for EGF repeats seven to nine

GAGCCATGCCACAAGAAGGTGTGCCCCATGGCACATGCCAGGCCAGCAGGCCAGGCTTCACCTCGCAGTGC
CAGGAAGGATGGATGGGGCCCTCTGTGACCAACGGACCAATGACCCCTTGCCCTGGAAATAATGCGTACATGGC
ACCTGCTGCCCATCAATGCGTTCTCCTACAGCTGTAAGTGCTGGAGGGCCATGGAGGTGTCCCTGTGATGAA
GAGGAGGATCTGTTAACCCATGCCAGGGCATCAAGTCAAGCATGGGAAGTGCAGGCTTCAGGTCTGGGCAG
CCCTACTGTGAATGCAGCATGGATACACGGGCACAGCTGTGATCGAGAAATC

75
150
225
300
353

$$398\frac{1}{4} - \frac{4341}{482}$$

Hybridisation Probe for the cysteine knot region

TCTTGTGAGGGGAAAGGATAAGAGATTATTAACAAAAGCAGCAGGGCTATGCTGCTTGCCAAACAACCAAGAAG
GTGTCCCCATTAGACTGAGGGTGGGTGTGAGGAGGGCAGTGCTGTGGACCGCTGAGGAGCAAGCGCGGAA
TACTCTTCGAATGCAGTGACGGCTCTCTTGTGGACGAGGTGAGAAAGTGGTGAAGTGGCTGTACGAGG
TGTGTGCC

75
150
225
234

11742-457

TABLE 6

PCR Primers for regions of Human Slit-1

PCR Primers for the first Leucine rich repeat region

Forward: 5' TGCCCGGCCAGTGTCTTGCTCGGGCAGC 3' 82 - 111
Reverse: 5' GTGAAACACTACAAGAAGGCCATAAA 3' 794 - 828 (Pc)

PCR Primers for the second Leucine rich repeat region

Forward: 5' TGCCCTGCCCTGTACCTGTAGCAACAAT 3' 82 - 85^b
Reverse: 5' AGCCAGATCCGAAAGCAGTCTCCACTTAA 3' 174 - 187 RL

PCR Primers for the third Leucine rich repeat region

Forward: 5' TGCCCTGAAAAGTGTCCGTGTGAAGGAACC 3' 1504 - 1533
Reverse: 5' GCGAGAAAGTGGGGAGCAACTATTGTCATC 3' 2137 - 2166

PCR Primers for the fourth Leucine rich repeat region

Forward: 5' TGTCTACTGAATGTACTTGTGGATACA 3' 2167 - 2196
Reverse: 5' GGGGTTACACTTAGCTAGAAATTGACATC 3' 2722 - 2751

PCR Primers for EGF repeats one to five

Forward: 5' TGCCTATCAAATCCGTGTAAAAATGATGGC 3' 2752 - 2781
Reverse: 5' AAACTCACAGAACAGCCACTGTAAACCTTC 3' 3248 - 3327

PCR Primers for the sixth EGF repeat and preceding spacer region

Forward: 5' TCTCCACCCATGGTCCTCCCTCGTACCGAC 3' 3329 - 3357
Reverse: 5' TTTCACACTTTCTCCCTGTAGCCAGGC 3' 7432 - 7461

PCR Primers for the 99aa spacer/G-loop region

Forward: 5' ATGGTTAGTGTGAATTATAAACAAAGA 3' 3462 - 3491
Reverse: 5' ACAGCCAGGCAAAATGCCTGTTGCATCGG 3' 3958 - 3987

PCR Primers for EGF repeats seven to nine

Forward: 5' GAGCCATGCCACAAGAAGGTGTGCCCCAT 3' 3988 - 4017
Reverse: 5' GATTCTCGATCACAGCTGTCCCCGTGTAT 3' 4132 - 4161

PCR Primers for the cysteine knot region

Forward: 5' TCTTGTGAGGGGAAAGGATAAGAGATTAT 3' 4712 - 4771
Reverse: 5' GGACACACACCTCGTACAGCCGCACTTCAC 3' 4546 - 4575